#18

SEQUENCE LISTING

<110> Kingsbury, G.
Leiby, K.

<120> COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF IMMUNE DISORDERS

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<141> 2001-07-06

<150> 60/155,862
<151> 1999-09-24

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<213> Homo sapiens

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<212> DNA
<213> Homo sapiens

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<210> 6
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<212> PRT
<213> Mus musculus

<400> 6

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Thr Tyr Pro Val Glu Trp Tyr Tyr Ser Asp Thr Asn Glu Ser Ile Pro
    50                  55                  60
Thr Gln Lys Arg Asn Arg Ile Phe Val Ser Arg Asp Arg Leu Lys Phe
65                  70                  75                  80
Leu Pro Ala Arg Val Glu Asp Ser Gly Ile Tyr Ala Cys Val Ile Arg
                85                  90                  95
Ser Pro Asn Leu Asn Lys Thr Gly Tyr Leu Asn Val Thr Ile His Lys
            100                 105                 110
Lys Pro Pro Ser Cys Asn Ile Pro Asp Tyr Leu Met Tyr Ser Thr Val
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Arg Gly Ser Asp Lys Asn Phe Lys Ile Thr Cys Pro Thr Ile Asp Leu
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Val Thr His Asp Asp Glu Gly Asp Tyr Thr Cys Gln Phe Thr His Ala
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Glu Asn Gly Thr Asn Tyr Ile Val Thr Ala Thr Arg Ser Phe Thr Val
        195                 200                 205
Glu Glu Lys Gly Phe Ser Met Phe Pro Val Ile Thr Asn Pro Pro Tyr
    210                 215                 220
Asn His Thr Met Glu Val Glu Ile Gly Lys Pro Ala Ser Ile Ala Cys
225                 230                 235                 240
Ser Ala Cys Phe Gly Lys Gly Ser His Phe Leu Ala Asp Val Leu Trp
                245                 250                 255
Gln Ile Asn Lys Thr Val Val Gly Asn Phe Gly Glu Ala Arg Ile Gln
            260                 265                 270
Glu Glu Glu Gly Arg Asn Glu Ser Ser Ser Asn Asp Met Asp Cys Leu
        275                 280                 285
Thr Ser Val Leu Arg Ile Thr Gly Val Thr Glu Lys Asp Leu Ser Leu
    290                 295                 300
Glu Tyr Asp Cys Leu Ala Leu Asn Leu His Gly Met Ile Arg His Thr
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<210> 7
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<212> PRT
<213> Mus musculus

<400> 7

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Thr Tyr Pro Val Glu Trp Tyr Tyr Ser Asp Thr Asn Glu Ser Ile Pro
    50                  55                  60
Thr Gln Lys Arg Asn Arg Ile Phe Val Ser Arg Asp Arg Leu Lys Phe
65                  70                  75                  80
Leu Pro Ala Arg Val Glu Asp Ser Gly Ile Tyr Ala Cys Val Ile Arg
                85                  90                  95
Ser Pro Asn Leu Asn Lys Thr Gly Tyr Leu Asn Val Thr Ile His Lys
            100                 105                 110
Lys Pro Pro Ser Cys Asn Ile Pro Asp Tyr Leu Met Tyr Ser Thr Val
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Arg Gly Ser Asp Lys Asn Phe Lys Ile Thr Cys Pro Thr Ile Asp Leu
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Tyr Asn Trp Thr Ala Pro Val Gln Trp Phe Lys Asn Cys Lys Ala Leu
145                 150                 155                 160
Gln Glu Pro Arg Phe Arg Ala His Arg Ser Tyr Leu Phe Ile Asp Asn
                165                 170                 175
Val Thr His Asp Asp Glu Gly Asp Tyr Thr Cys Gln Phe Thr His Ala
            180                 185                 190
Glu Asn Gly Thr Asn Tyr Ile Val Thr Ala Thr Arg Ser Phe Thr Val
        195                 200                 205
Glu Glu Lys Gly Phe Ser Met Phe Pro Val Ile Thr Asn Pro Pro Tyr
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Asn His Thr Met Glu Val Glu Ile Gly Lys Pro Ala Ser Ile Ala Cys
225                 230                 235                 240
Ser Ala Cys Phe Gly Lys Gly Ser His Phe Leu Ala Asp Val Leu Trp
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Gln Ile Asn Lys Thr Val Val Gly Asn Phe Gly Glu Ala Arg Ile Gln
            260                 265                 270
Glu Glu Glu Gly Arg Asn Glu Ser Ser Ser Asn Asp Met Asp Cys Leu
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Thr Ser Val Leu Arg Ile Thr Gly Val Thr Glu Lys Asp Leu Ser Leu
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Glu Tyr Asp Cys Leu Ala Leu Asn Leu His Gly Met Ile Arg His Thr
305                 310                 315                 320
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Gln Val Phe Val Leu Ala Pro His Met Met His Ser Lys Glu Phe Ala
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Tyr Glu Gln Glu Ile Ala Leu His Ser Ala Leu Ile Gln Asn Asn Ser
465                 470                 475                 480
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Gln Val Gly Asp Leu Gln Asp Ser Leu Gln His Leu Val Lys Ile Gln
            500                 505                 510
Gly Thr Ile Lys Trp Arg Glu Asp His Val Ala Asp Lys Gln Ser Leu
        515                 520                 525
Ser Ser Lys Phe Trp Lys His Val Arg Tyr Gln Met Pro Val Pro Glu
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Arg Ala Ser Lys Thr Ala Ser Val Ala Ala Pro Leu Ser Gly Lys Ala
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<210> 8
<211> 556
<212> PRT
<213> Homo sapiens

<400> 8

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            20                  25                  30
Ile Val Arg Cys Pro Arg Gln Gly Lys Pro Ser Tyr Thr Val Asp Trp
        35                  40                  45
Tyr Tyr Ser Gln Thr Asn Lys Ser Ile Pro Thr Gln Glu Arg Asn Arg
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Val Phe Ala Ser Gly Gln Leu Leu Lys Phe Leu Pro Ala Glu Val Ala
65                  70                  75                  80
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Asp Ser Gly Ile Tyr Thr Cys Ile Val Arg Ser Pro Thr Phe Asn Arg
                 85                  90                  95
Thr Gly Tyr Ala Asn Val Thr Ile Tyr Lys Lys Gln Ser Asp Cys Asn
            100                 105                 110
Val Pro Asp Tyr Leu Met Tyr Ser Thr Val Ser Gly Ser Glu Lys Asn
        115                 120                 125
Ser Lys Ile Tyr Cys Pro Thr Ile Asp Leu Tyr Asn Trp Thr Ala Pro
    130                 135                 140
Leu Glu Trp Phe Lys Asn Cys Gln Ala Leu Gln Gly Ser Arg Tyr Arg
145                 150                 155                 160
Ala His Lys Ser Phe Leu Val Ile Asp Asn Val Met Thr Glu Asp Ala
                165                 170                 175
Gly Asp Tyr Thr Cys Lys Phe Ile His Asn Glu Asn Gly Ala Asn Tyr
            180                 185                 190
Ser Val Thr Ala Thr Arg Ser Phe Thr Val Lys Asp Glu Gln Gly Phe
        195                 200                 205
Ser Leu Phe Pro Val Ile Gly Ala Pro Ala Gln Asn Glu Ile Lys Glu
    210                 215                 220
Val Glu Ile Gly Lys Asn Ala Asn Leu Thr Cys Ser Ala Cys Phe Gly
225                 230                 235                 240
Lys Gly Thr Gln Phe Leu Ala Ala Val Leu Trp Gln Leu Asn Gly Thr
                245                 250                 255
Lys Ile Thr Asp Phe Gly Glu Pro Arg Ile Gln Gln Glu Glu Gly Gln
            260                 265                 270
Asn Gln Ser Phe Ser Asn Gly Leu Ala Cys Leu Asp Met Val Leu Arg
        275                 280                 285
Ile Ala Asp Val Lys Glu Glu Asp Leu Leu Leu Gln Tyr Asp Cys Leu
    290                 295                 300
Ala Leu Asn Leu His Gly Leu Arg Arg His Thr Val Arg Leu Ser Arg
305                 310                 315                 320
Lys Asn Pro Ile Asp His His Ser Ile Tyr Cys Ile Ile Ala Val Cys
                325                 330                 335
Ser Val Phe Leu Met Leu Ile Asn Val Leu Val Ile Ile Leu Lys Met
            340                 345                 350
Phe Trp Ile Glu Ala Thr Leu Leu Trp Arg Asp Ile Ala Lys Pro Tyr
        355                 360                 365
Lys Thr Arg Asn Asp Gly Lys Leu Tyr Asp Ala Tyr Val Val Tyr Pro
    370                 375                 380
Arg Asn Tyr Lys Ser Ser Thr Asp Gly Ala Ser Arg Val Glu His Phe
385                 390                 395                 400
Val His Gln Ile Leu Pro Asp Val Leu Glu Asn Lys Cys Gly Tyr Thr
                405                 410                 415
Leu Cys Ile Tyr Gly Arg Asp Met Leu Pro Gly Glu Asp Val Val Thr
            420                 425                 430
Ala Val Glu Thr Asn Ile Arg Lys Ser Arg Arg His Ile Phe Ile Leu
        435                 440                 445
Thr Pro Gln Ile Thr His Asn Lys Glu Phe Ala Tyr Glu Gln Glu Val
    450                 455                 460
Ala Leu His Cys Ala Leu Ile Gln Asn Asp Ala Lys Val Ile Leu Ile
465                 470                 475                 480
Glu Met Glu Ala Leu Ser Glu Leu Asp Met Leu Gln Ala Glu Ala Leu
                485                 490                 495
Gln Asp Ser Leu Gln His Leu Met Lys Val Gln Gly Thr Ile Lys Trp
            500                 505                 510
Arg Glu Asp His Ile Ala Asn Lys Arg Ser Leu Asn Ser Lys Phe Trp
        515                 520                 525
Lys His Val Arg Tyr Gln Met Pro Val Pro Ser Lys Ile Pro Arg Lys
    530                 535                 540
Ala Ser Ser Leu Thr Pro Leu Ala Ala Gln Lys Gln
545                 550                 555
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<210> 9
<211> 328
<212> PRT
<213> Homo sapiens

<400> 9

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Met Gly Phe Trp Ile Leu Ala Ile Leu Thr Ile Leu Met Tyr Ser Thr
 1               5                  10                  15
Ala Ala Lys Phe Ser Lys Gln Ser Trp Gly Leu Glu Asn Glu Ala Leu
            20                  25                  30
Ile Val Arg Cys Pro Arg Gln Gly Lys Pro Ser Tyr Thr Val Asp Trp
        35                  40                  45
Tyr Tyr Ser Gln Thr Asn Lys Ser Ile Pro Thr Gln Glu Arg Asn Arg
    50                  55                  60
Val Phe Ala Ser Gly Gln Leu Leu Lys Phe Leu Pro Ala Glu Val Ala
65                  70                  75                  80
Asp Ser Gly Ile Tyr Thr Cys Ile Val Arg Ser Pro Thr Phe Asn Arg
                85                  90                  95
Thr Gly Tyr Ala Asn Val Thr Ile Tyr Lys Lys Gln Ser Asp Cys Asn
            100                 105                 110
Val Pro Asp Tyr Leu Met Tyr Ser Thr Val Ser Gly Ser Glu Lys Asn
        115                 120                 125
Ser Lys Ile Tyr Cys Pro Thr Ile Asp Leu Tyr Asn Trp Thr Ala Pro
    130                 135                 140
Leu Glu Trp Phe Lys Asn Cys Gln Ala Leu Gln Gly Ser Arg Tyr Arg
145                 150                 155                 160
Ala His Lys Ser Phe Leu Val Ile Asp Asn Val Met Thr Glu Asp Ala
                165                 170                 175
Gly Asp Tyr Thr Cys Lys Phe Ile His Asn Glu Asn Gly Ala Asn Tyr
            180                 185                 190
Ser Val Thr Ala Thr Arg Ser Phe Thr Val Lys Asp Glu Gln Gly Phe
        195                 200                 205
Ser Leu Phe Pro Val Ile Gly Ala Pro Ala Gln Asn Glu Ile Lys Glu
    210                 215                 220
Val Glu Ile Gly Lys Asn Ala Asn Leu Thr Cys Ser Ala Cys Phe Gly
225                 230                 235                 240
Lys Gly Thr Gln Phe Leu Ala Ala Val Leu Trp Gln Leu Asn Gly Thr
                245                 250                 255
Lys Ile Thr Asp Phe Gly Glu Pro Arg Ile Gln Gln Glu Glu Gly Gln
            260                 265                 270
Asn Gln Ser Phe Ser Asn Gly Leu Ala Cys Leu Asp Met Val Leu Arg
        275                 280                 285
Ile Ala Asp Val Lys Glu Glu Asp Leu Leu Leu Gln Tyr Asp Cys Leu
    290                 295                 300
Ala Leu Asn Leu His Gly Leu Arg Arg His Thr Val Arg Leu Ser Arg
305                 310                 315                 320
Lys Asn Pro Ser Lys Glu Cys Phe
                325
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<210> 10
<211> 1680
<212> DNA
<213> Homo sapiens

<400> 10

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cttagctccg tcactgactc caagttcatc ccctctgtct ttcagtttgg ttgagatata      60
ggctactctt cccaactcag tcttgaagag tatcaccaac tgcctcatgt gtggtgacct     120
tcactgttgt atgccagtga ctcatctgga gtaatctcaa caacgagtta ccaatacttg     180
ctcttgattg ataaacagaa tggggttttg gatcttagca attctcacaa ttctcatgta     240
ttccacagca gcaaagttta gtaaacaatc atggggcctg gaaaatgagg ctttaattgt     300
aagatgtcct agacaaggaa aacctagtta caccgtggat tggtattact cacaaacaaa     360
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caaaagtatt cccactcagg aaagaaatcg tgtgtttgcc tcaggccgac ttctgaagtt 420
tctaccagct gaagttgctg attctggtat ttatacctgt attgtcagaa gtcccacatt 480
caataggact ggatatgcga atgtcaccat atataaaaaa caatcagatt gcaatgttcc 540
agattatttg atgtattcaa cagtatctgg atcagaaaaa aattccaaaa tttattgtcc 600
taccattgac ctctacaact ggacagcacc tcttgagtgg tttaagaatt gtcaggctct 660
tcaaggatca aggtacaggg cgcacaagtc atttttggtc attgataatg tgatgactga 720
ggacgcaggt gattacacct gtaaatttat acacaatgaa aatggagcca attatagtgt 780
gacggcgacc aggtccttca cggtcaaggt ttggtgtcag agtttctgca aattaaaaaa 840
gagcttaatc tttagtaata ctcattggat tcaaagtcta atgagaggct ttgtgatggt 900
atactatggt gtacataaat gttgtcgagt ggtttttaat ctttgtttgc aatactttca 960
acatcatcaa tggccttgaa tgagcaaggc ttttctctgt ttccagtaat cggagcccct 1020
gcacaaaatg aaataaagga agtggaaatt ggaaaaaacg caaacctaac ttgctctgct 1080
tgttttggaa aaggcactca gttcttggct gccgtcctgt ggcagcttaa tggaacaaaa 1140
attacagact ttggtgaacc aagaattcaa caagaggaag ggcaaaatca aagtttcagc 1200
aatgggctgg cttgtctaga catggtttta agaatagctg acgtgaagga agaggattta 1260
ttgctgcagt acgactgtct ggccctgaat ttgcatggct tgagaaggca caccgtaaga 1320
ctaagtagga aaaatccaag taaggagtgt ttctgagact ttgatcacct gaactttctc 1380
tagcaagtgt aagcagaatg gagtgtggtt ccaagagatc catcaagaca atgggaatgg 1440
cctgtgccat aaaatgtgct tctcttcttc gggatgttgt ttgctgtctg atctttgtag 1500
actgttcctg tttgctggga gcttctctgc tgcttaaatt gttcgtcctc ccccactccc 1560
tcctatcgtt ggtttgtcta gaacactcag ctgcttcttt ggtcatcctt gttttctaac 1620
tttatgaact ccctctgtgt cactgtatgt gaaaggaaat gcaccaacaa ccgaaaactg 1680

<210> 11
<211> 259
<212> PRT
<213> Homo sapiens

<400> 11

Met	Gly	Phe	Trp	Ile	Leu	Ala	Ile	Leu	Thr	Ile	Leu	Met	Tyr	Ser	Thr
1				5					10					15	
Ala	Ala	Lys	Phe	Ser	Lys	Gln	Ser	Trp	Gly	Leu	Glu	Asn	Glu	Ala	Leu
			20					25					30		
Ile	Val	Arg	Cys	Pro	Arg	Gln	Gly	Lys	Pro	Ser	Tyr	Thr	Val	Asp	Trp
		35					40					45			
Tyr	Tyr	Ser	Gln	Thr	Asn	Lys	Ser	Ile	Pro	Thr	Gln	Glu	Arg	Asn	Arg
	50					55					60				
Val	Phe	Ala	Ser	Gly	Arg	Leu	Leu	Lys	Phe	Leu	Pro	Ala	Glu	Val	Ala
65					70					75					80
Asp	Ser	Gly	Ile	Tyr	Thr	Cys	Ile	Val	Arg	Ser	Pro	Thr	Phe	Asn	Arg
				85					90					95	
Thr	Gly	Tyr	Ala	Asn	Val	Thr	Ile	Tyr	Lys	Lys	Gln	Ser	Asp	Cys	Asn
			100					105					110		
Val	Pro	Asp	Tyr	Leu	Met	Tyr	Ser	Thr	Val	Ser	Gly	Ser	Glu	Lys	Asn
		115					120					125			
Ser	Lys	Ile	Tyr	Cys	Pro	Thr	Ile	Asp	Leu	Tyr	Asn	Trp	Thr	Ala	Pro
	130					135					140				
Leu	Glu	Trp	Phe	Lys	Asn	Cys	Gln	Ala	Leu	Gln	Gly	Ser	Arg	Tyr	Arg
145					150					155					160
Ala	His	Lys	Ser	Phe	Leu	Val	Ile	Asp	Asn	Val	Met	Thr	Glu	Asp	Ala
				165					170					175	
Gly	Asp	Tyr	Thr	Cys	Lys	Phe	Ile	His	Asn	Glu	Asn	Gly	Ala	Asn	Tyr
			180					185					190		
Ser	Val	Thr	Ala	Thr	Arg	Ser	Phe	Thr	Val	Lys	Val	Trp	Cys	Gln	Ser
		195					200					205			
Phe	Cys	Lys	Leu	Lys	Lys	Ser	Leu	Ile	Phe	Ser	Asn	Thr	His	Trp	Ile
	210					215					220				
Gln	Ser	Leu	Met	Arg	Gly	Phe	Val	Met	Val	Tyr	Tyr	Gly	Val	His	Lys
225					230					235					240
Cys	Cys	Arg	Val	Val	Phe	Asn	Leu	Cys	Leu	Gln	Tyr	Phe	Gln	His	His
				245					250					255	

Gln Trp Pro

<210> 12
<211> 1210
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (84)...(557)

<400> 12

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cttgctcttg attgataaac aga atg ggg ttt tgg atc tta gca att ctc aca    113
                          Met Gly Phe Trp Ile Leu Ala Ile Leu Thr
                           1               5                  10

att ctc atg tat tcc aca gca gca aag ttt agt aaa caa tca tgg ggc      161
Ile Leu Met Tyr Ser Thr Ala Ala Lys Phe Ser Lys Gln Ser Trp Gly
                 15                  20                  25

ctg gaa aat gag gct tta att gta aga tgt cct aga caa gga aaa cct      209
Leu Glu Asn Glu Ala Leu Ile Val Arg Cys Pro Arg Gln Gly Lys Pro
             30                  35                  40

agt tac acc gtg gat tgg tat tac tca caa aca aac aaa agt att ccc      257
Ser Tyr Thr Val Asp Trp Tyr Tyr Ser Gln Thr Asn Lys Ser Ile Pro
         45                  50                  55

act cag gaa aga aat cgt gtg ttt gcc tca ggc caa ctt ctg aag ttt      305
Thr Gln Glu Arg Asn Arg Val Phe Ala Ser Gly Gln Leu Leu Lys Phe
     60                  65                  70

cta cca gct gca gtt gct gat tct ggt att tat acc tgt att gtc aga      353
Leu Pro Ala Ala Val Ala Asp Ser Gly Ile Tyr Thr Cys Ile Val Arg
 75                  80                  85                  90

agt ccc aca ttc aat agg act gga tat gcg aat gtc acc ata tat aaa      401
Ser Pro Thr Phe Asn Arg Thr Gly Tyr Ala Asn Val Thr Ile Tyr Lys
                 95                 100                 105

aaa caa tca gat tgc aat gtt cca gat tat ttg atg tat tca aca gta      449
Lys Gln Ser Asp Cys Asn Val Pro Asp Tyr Leu Met Tyr Ser Thr Val
             110                 115                 120

tct gga tca gaa aaa aat tcc aaa att tat tgt cct acc att gac ctc      497
Ser Gly Ser Glu Lys Asn Ser Lys Ile Tyr Cys Pro Thr Ile Asp Leu
         125                 130                 135

tac aac tgg aca gca cct ctt gag tgg ttt aag atg agc aag gct ttt      545
Tyr Asn Trp Thr Ala Pro Leu Glu Trp Phe Lys Met Ser Lys Ala Phe
    140                 145                 150

ctc tgt ttc cag taatcggagc ccctgcacaa aatgaaataa aggaagtgga          597
Leu Cys Phe Gln
155

aattggcact cagttcttgg ctgccgtcct gtggcagctt aatggaacaa aaattacaga    657
ctttggtgaa ccaagaattc aacaagagga agggcaaaat caaagtttca gcaatgggct    717
ggcttgtcta gacatggttt taagaatagc tgacgtgaag gaagaggatt tattgctgca    777
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gtacgactgt ctggccctga atttgcatgg cttgagaagg cacaccgtaa gactaagtag    837
gaaaaatcca agtaaggagt gtttctgaga ctttgatcac ctgaactttc tctagcaagt    897
gtaagcagaa tggagtgtgg ttccaagaga tccatcaaga caatgggaat ggcctgtgcc    957
ataaaatgtg cttctcttct tcgggatgtt gtttgctgtc tgatctttgt agactgttcc   1017
tgtttgctgg gagcttctct gctgcttaaa ttgttcgtcc tcccccactc cctcctatcg   1077
ttggtttgtc tagaacactc agctgcttct ttggtcatcc ttgttttcta actttatgaa   1137
ctcctctgt gtcactgtat gtgaaaggaa atgcaccaac aaccgtaaaa aaaaaaaaaa   1197
aagggcggcc gct                                                     1210
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<210> 13
<211> 158
<212> PRT
<213> Homo sapiens

<400> 13

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Met Gly Phe Trp Ile Leu Ala Ile Leu Thr Ile Leu Met Tyr Ser Thr
 1               5                  10                  15
Ala Ala Lys Phe Ser Lys Gln Ser Trp Gly Leu Glu Asn Glu Ala Leu
            20                  25                  30
Ile Val Arg Cys Pro Arg Gln Gly Lys Pro Ser Tyr Thr Val Asp Trp
        35                  40                  45
Tyr Tyr Ser Gln Thr Asn Lys Ser Ile Pro Thr Gln Glu Arg Asn Arg
    50                  55                  60
Val Phe Ala Ser Gly Gln Leu Leu Lys Phe Leu Pro Ala Ala Val Ala
65                  70                  75                  80
Asp Ser Gly Ile Tyr Thr Cys Ile Val Arg Ser Pro Thr Phe Asn Arg
                85                  90                  95
Thr Gly Tyr Ala Asn Val Thr Ile Tyr Lys Lys Gln Ser Asp Cys Asn
            100                 105                 110
Val Pro Asp Tyr Leu Met Tyr Ser Thr Val Ser Gly Ser Glu Lys Asn
        115                 120                 125
Ser Lys Ile Tyr Cys Pro Thr Ile Asp Leu Tyr Asn Trp Thr Ala Pro
    130                 135                 140
Leu Glu Trp Phe Lys Met Ser Lys Ala Phe Leu Cys Phe Gln
145                 150                 155
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<210> 14
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> sense primer

<400> 14

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ttgccataga gagacctc                                                18
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<210> 15
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> antisense primer

<400> 15

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tgctgtccaa ttatacagg                                               19
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<210> 16
<211> 22
<212> DNA

<213> Artificial Sequence

<220>
<223> sense primer

<400> 16
gaacacggca ttgtcactaa ct 22

<210> 17
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> antisense primer

<400> 17
cctcatagat gggcactgtg t 21

<210> 18
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> forward primer

<400> 18
tgtgacggcg accaggt 17

<210> 19
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> reverse primer

<400> 19
tctctgtttc cagtaatcgg agc 23

<210> 20
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> TaqMan probe

<400> 20
ttcacggtca aggatgagca agcctt 26

<210> 21
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> forward primer

<400> 21

cacccccact gaaaaagatg a 21

<210> 22
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> reverse primer

<400> 22
cttaactatc ttgggctgtg acaaag 26

<210> 23
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> TaqMan probe

<400> 23
tatgcctgcc gtgtgaacca cgtg 24

<210> 24
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> 5' oligonucleotide

<400> 24
ccgcgggtac cagtaaatcg tcctggggtg g 31

<210> 25
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> 3' oligonucleotide

<400> 25
aaataaagga tccctacatc cagcaactat gtagta 36

<210> 26
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> 5' oligonucleotide

<400> 26
gaacacacta gtactatcct gtgccattgc catagaga 38

<210> 27
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> 3' oligonucleotide

<400> 27
ggaatattgg gcccttggat cccaagtctg cacacctgca ctcc 44

<210> 28
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> 5' oligonucleotide

<400> 28
gtaaatcgtc ctggggtctg g 21

<210> 29
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> 3' oligonucleotide

<400> 29
ccttctgata acacaagcat aaatc 25

<210> 30
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 30
acggagggca gtaaatc 17

<210> 31
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 31
cagccaagaa gtgagagc 18

<210> 32
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 32
tgttgccgga atccagcctc ag 22

<210> 33
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 33
gtcccccacc cccagataca acc 23